Sequence Listing

<110> Desnoyers,Luc
Eaton,Dan L.
Goddard,Audrey
Godowski,Paul J.
Gurney,Austin L.
Pan,James
Stewart,Timothy A.
Watanabe,Colin K.
Wood,William I.
Zhang,Zemin

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Glu	Lys	Gly	Tyr	Pro	Gly	Ile	Pro	Pro	Glu	Leu	Gln	Ile	Ala	Phe
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155 160 165

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170 175 180

Tyr Leu Met His Asn Gly Asn Thr Val Phe Ser Met Tyr Ser Tyr
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Glu Met Lys Gly Lys Ser Asp Thr Ser Ser Asn His Ala Val Leu
200 205 210

Lys Leu Ala Lys Gly Asp Glu Val Trp Leu Arg Met Gly Asn Gly
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Pro Thr Tyr Cys Leu Glu Tyr Lys Asn Val Pro Thr Asp Ile Asn
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Phe Ala Asn Ala Val Ser Asp Ala Leu Asp Ser Phe Lys Ser Gly
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Arg Ala Asp Leu Ala Ala Ile Tyr His Glu Arg Ile Asp Val Glu
185 190 195

Gly His His Tyr Gly Pro Ala Ser Pro Gln Arg Lys Asp Ala Leu
200 205 210

Lys Ala Val Asp Thr Val Leu Lys Tyr Met Thr Lys Trp Ile Gln
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Glu Arg Gly Leu Gln Asp Arg Leu Asn Val Ile Ile Phe Ser Asp
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His Gly Met Thr Asp Ile Phe Trp Met Asp Lys Val Ile Glu Leu
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260 265 270

Gly Pro Val Val Ser Leu Trp Pro Ala Pro Gly Lys His Ser Glu
275 280 285

Ile Tyr Asn Lys Leu Ser Thr Val Glu His Met Thr Val Tyr Glu
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365 370 375

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380 385 390

Val Met Cys Asn Val Val Gly Ile Thr Pro Leu Pro Asn Asn Gly
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 Ile Ser Pro Trp Arg Tyr Arg Val Asp Thr Asp Glu Asp Arg Tyr
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35 40 45

His Cys Val Thr Thr Ala Thr Arg Val Leu Ser Asn Thr Glu Asp
50 55 60

Leu Pro Leu Val Thr Lys Met Cys His Ile Gly Cys Pro Asp Ile
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Thr Ser Leu Cys Asn His Asp
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aaacctcctc aaacatttta cttagaggca aggattgtct aatttcaatt 1900

gtgcaagaca tgtgccttat aattattttt agcttaaaat taaacagatt 1950

ttgtaataat gtaactttgt taataggtgc ataaacacta atgcagtcaa 2000

tttgaacaaa agaagtgaca tacacaatat aaatcatatg tcttcacacg 2050

ttgcctatat aatgagaagc agctctctga gggttctgaa atcaatgtgg 2100

tccctctctt gcccactaaa caaagatggt tgttcggggt ttgggattga 2150

cactggaggc agatagttgc aaagttagtc taaggtttcc ctagctgtat 2200

ttagcctctg actatattag tatacaaaga ggtcatgtgg ttgagaccag 2250

gtgaatagtc actatcagtg tggagacaag cacagcacac agacatttta 2300

ggaaggaaag gaactacgaa atcgtgtgaa aatgggttgg aacccatcag 2350

tgatcgcata ttcattgatg agggtttgct tgagatagaa aatggtggct 2400

cctttctgtc ttatctccta gtttcttcaa tgcttacgcc ttgttcttct 2450

caagagaaag ttgtaactct ctggtcttca tatgtccctg tgctcctttt 2500

aaccaaataa agagttcttg tttctggggg aaaaaaaaaa aaaaaaaaaa 2550

aaaaaaaaaa aaaaaaaaaa 2570

<210> 18
<211> 273
<212> PRT
<213> Homo Sapien

<400> 18

Met Ser Arg Val Val Ser Leu Leu Leu Gly Ala Ala Leu Leu Cys
1 5 10 15

Gly His Gly Ala Phe Cys Arg Arg Val Val Ser Gly Gln Lys Val
20 25 30

Cys Phe Ala Asp Phe Lys His Pro Cys Tyr Lys Met Ala Tyr Phe
35 40 45

His Glu Leu Ser Ser Arg Val Ser Phe Gln Glu Ala Arg Leu Ala
50 55 60

Cys Glu Ser Glu Gly Gly Val Leu Leu Ser Leu Glu Asn Glu Ala
65 70 75

Glu Gln Lys Leu Ile Glu Ser Met Leu Gln Asn Leu Thr Lys Pro
80 85 90

Gly Thr Gly Ile Ser Asp Gly Asp Phe Trp Ile Gly Leu Trp Arg
95 100 105

Asn Gly Asp Gly Gln Thr Ser Gly Ala Cys Pro Asp Leu Tyr Gln
110 115 120

Trp Ser Asp Gly Ser Asn Ser Gln Tyr Arg Asn Trp Tyr Thr Asp
125 130 135

Glu Pro Ser Cys Gly Ser Glu Lys Cys Val Val Met Tyr His Gln
140 145 150

Pro Thr Ala Asn Pro Gly Leu Gly Gly Pro Tyr Leu Tyr Gln Trp
155 160 165

Asn Asp Asp Arg Cys Asn Met Lys His Asn Tyr Ile Cys Lys Tyr

170 175 180

Glu Pro Glu Ile Asn Pro Thr Ala Pro Val Glu Lys Pro Tyr Leu
185 190 195

Thr Asn Gln Pro Gly Asp Thr His Gln Asn Val Val Val Thr Glu
200 205 210

Ala Gly Ile Ile Pro Asn Leu Ile Tyr Val Val Ile Pro Thr Ile
215 220 225

Pro Leu Leu Leu Leu Ile Leu Val Ala Phe Gly Thr Cys Cys Phe
230 235 240

Gln Met Leu His Lys Ser Lys Gly Arg Thr Lys Thr Ser Pro Asn
245 250 255

Gln Ser Thr Leu Trp Ile Ser Lys Ser Thr Arg Lys Glu Ser Gly
260 265 270

Met Glu Val

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
caccaaccaa ctgccaatcc tggc 24

<210> 20
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
accacattct gatgggtgtc tcctgg 26

<210> 21
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
gggtccctac ctttaccagt ggaatgatga caggtgtaac atgaagcac 49

<210> 22
<211> 3824

<212> DNA
<213> Homo Sapien

<400> 22
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gtctgtctgc tcctggcatg ccctgccaca gccactgggc ccgaagttgc 100

tcagcctgaa gtagacacca ccctgggtcg tgtgcgaggc cggcaggtgg 150

gcgtgaaggg cacagaccgc cttgtgaatg tctttctggg cattccattt 200

gcccagccgc cactgggccc tgaccggttc tcagccccac acccagcaca 250

gccctgggag ggtgtgcggg atgccagcac tgcgccccca atgtgcctac 300

aagacgtgga gagcatgaac agcagcagat ttgtcctcaa cggaaaacag 350

cagatcttct ccgtttcaga ggactgcctg gtcctcaacg tctatagccc 400

agctgaggtc cccgcagggt ccggtaggcc ggtcatggta tgggtccatg 450

gaggcgctct gataactggc gctgccacct cctacgatgg atcagctctg 500

gctgcctatg gggatgtggt cgtggttaca gtccagtacc gccttggggt 550

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tcctagatgt ggtagctgct ttgcgctggg tgcaagaaaa catcgccccc 650

ttcgggggtg acctcaactg tgtcactgtc tttggtggat ctgccggtgg 700

gagcatcatc tctggcctgg tcctgtcccc agtggctgca gggctgttcc 750

acagagccat cacacagagt ggggtcatca ccaccccagg gatcatcgac 800

tctcaccctt ggcccctagc tcagaaaatc gcaaacacct tggcctgcag 850

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gccacgggcc ggacagaagt tcagggaggc ctggatgcag ttctggtcag 1650

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cagacctgac cctcaccaat tccagcccct gaccctcagg acgctggatg 2550

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agaggttttc agatggaagt gagaggtgac agtgtgctgg cagccctcac 2800

agccctcgct tgctctccct gccgcctctg cctgggctcc cactttggca 2850

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gctcgatttc tcgctgggcc ttagctgcct ccccgcgggg cagggctcgg 3150

gacctgcagc cctccatgcc tgaccctccc cccacccccc gtgggctcct 3200

gtgcggccgg agcctcccca aggagcgccg ccccctgctc cacagcgccc 3250

agtcccatcg accacccaag ggctgaggag tgcgggtgca cagcgcggga 3300

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ccagctgggc tcctgagtct ggtggggact tggagaacct ttatgtctag 3400

ctaagggatt gtaaatacac cgatgggcac tctgtatcta gctcaaggtt 3450

tgtaaacaca ccaatcagca ccctgtgtct agctcagtgt ttgtgaatgc 3500

accaatccac actctgtatc tggctactct ggtggggact tggagaacct 3550

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ttgtgtctag ctcagggatc gtaaacgcac caatcagcac cctgtcaaaa 3650

cagaccactt gactctctgt aaaatggacc aatcagcagg atgtgggtgg 3700

ggcgagacaa gagaataaaa gcaggctgcc tgagccagca gtgacaaccc 3750

ccctcgggtc ccctcccacg ccgtggaagc tttgttcttt cgctctttgc 3800

aataaatctt gctactgccc aaaa 3824

<210> 23
<211> 571
<212> PRT
<213> Homo Sapien

<400> 23

Met Glu Arg Ala Val Arg Val Glu Ser Gly Val Leu Val Gly Val
1 5 10 15

Val Cys Leu Leu Leu Ala Cys Pro Ala Thr Ala Thr Gly Pro Glu
20 25 30

Val Ala Gln Pro Glu Val Asp Thr Thr Leu Gly Arg Val Arg Gly
35 40 45

Arg Gln Val Gly Val Lys Gly Thr Asp Arg Leu Val Asn Val Phe

50 55 60

Leu Gly Ile Pro Phe Ala Gln Pro Pro Leu Gly Pro Asp Arg Phe
65 70 75

Ser Ala Pro His Pro Ala Gln Pro Trp Glu Gly Val Arg Asp Ala
80 85 90

Ser Thr Ala Pro Pro Met Cys Leu Gln Asp Val Glu Ser Met Asn
95 100 105

Ser Ser Arg Phe Val Leu Asn Gly Lys Gln Gln Ile Phe Ser Val
110 115 120

Ser Glu Asp Cys Leu Val Leu Asn Val Tyr Ser Pro Ala Glu Val
125 130 135

Pro Ala Gly Ser Gly Arg Pro Val Met Val Trp Val His Gly Gly
140 145 150

Ala Leu Ile Thr Gly Ala Ala Thr Ser Tyr Asp Gly Ser Ala Leu
155 160 165

Ala Ala Tyr Gly Asp Val Val Val Val Thr Val Gln Tyr Arg Leu
170 175 180

Gly Val Leu Gly Phe Phe Ser Thr Gly Asp Glu His Ala Pro Gly
185 190 195

Asn Gln Gly Phe Leu Asp Val Val Ala Ala Leu Arg Trp Val Gln
200 205 210

Glu Asn Ile Ala Pro Phe Gly Gly Asp Leu Asn Cys Val Thr Val
215 220 225

Phe Gly Gly Ser Ala Gly Gly Ser Ile Ile Ser Gly Leu Val Leu
230 235 240

Ser Pro Val Ala Ala Gly Leu Phe His Arg Ala Ile Thr Gln Ser
245 250 255

Gly Val Ile Thr Thr Pro Gly Ile Ile Asp Ser His Pro Trp Pro
260 265 270

Leu Ala Gln Lys Ile Ala Asn Thr Leu Ala Cys Ser Ser Ser Ser
275 280 285

Pro Ala Glu Met Val Gln Cys Leu Gln Gln Lys Glu Gly Glu Glu
290 295 300

Leu Val Leu Ser Lys Lys Leu Lys Asn Thr Ile Tyr Pro Leu Thr
305 310 315

Val Asp Gly Thr Val Phe Pro Lys Ser Pro Lys Glu Leu Leu Lys
320 325 330

Glu Lys Pro Phe His Ser Val Pro Phe Leu Met Gly Val Asn Asn
335 340 345

His Glu Phe Ser Trp Leu Ile Pro Arg Gly Trp Gly Leu Leu Asp
350 355 360

Thr Met Glu Gln Met Ser Arg Glu Asp Met Leu Ala Ile Ser Thr
365 370 375

Pro Val Leu Thr Ser Leu Asp Val Pro Pro Glu Met Met Pro Thr
380 385 390

Val Ile Asp Glu Tyr Leu Gly Ser Asn Ser Asp Ala Gln Ala Lys
395 400 405

Cys Gln Ala Phe Gln Glu Phe Met Gly Asp Val Phe Ile Asn Val
410 415 420

Pro Thr Val Ser Phe Ser Arg Tyr Leu Arg Asp Ser Gly Ser Pro
425 430 435

Val Phe Phe Tyr Glu Phe Gln His Arg Pro Ser Ser Phe Ala Lys
440 445 450

Ile Lys Pro Ala Trp Val Lys Ala Asp His Gly Ala Glu Gly Ala
455 460 465

Phe Val Phe Gly Gly Pro Phe Leu Met Asp Glu Ser Ser Arg Leu
470 475 480

Ala Phe Pro Glu Ala Thr Glu Glu Glu Lys Gln Leu Ser Leu Thr
485 490 495

Met Met Ala Gln Trp Thr His Phe Ala Arg Thr Gly Asp Pro Asn
500 505 510

Ser Lys Ala Leu Pro Pro Trp Pro Gln Phe Asn Gln Ala Glu Gln
515 520 525

Tyr Leu Glu Ile Asn Pro Val Pro Arg Ala Gly Gln Lys Phe Arg
530 535 540

Glu Ala Trp Met Gln Phe Trp Ser Glu Thr Leu Pro Ser Lys Ile
545 550 555

Gln Gln Trp His Gln Lys Gln Lys Asn Arg Lys Ala Gln Glu Asp
560 565 570

Leu

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
gcaaagctct gcctccttgg cc 22

<210> 25
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
gggtggactg tgctctaatg gacgc 25

<210> 26
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
cgtggcactg ggttgatc 18

<210> 27
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
gatgcagttc tggtcagaga cgctccccag caagatacaa cagtg 45

<210> 28
<211> 1342
<212> DNA
<213> Homo Sapien

<400> 28
catggagcct cttgcagctt acccgctaaa atgttccggg cccagagcaa 50

aggtatttgc agttttgctg tctatagttc tatgcacagt aacgctattt 100

cttctacaac taaaattcct caaacctaaa atcaacagct tttatgcctt 150

tgaagtgaag gatgcaaaag gaagaactgt ttctctggaa aagtataaag 200

gcaaagtttc actagttgta aacgtggcca gtgactgcca actcacagac 250

agaaattact tagggctgaa ggaactgcac aaagagtttg gaccatccca 300

cttcagcgtg ttggcttttc cctgcaatca gtttggagaa tcggagcccc 350

gcccaagcaa ggaagtagaa tcttttgcaa gaaaaaacta cggagtaact 400

ttccccatct tccacaagat taagattcta ggatctgaag gagaacctgc 450

atttagattt cttgttgatt cttcaaagaa ggaaccaagg tggaattttt 500

ggaagtatct tgtcaaccct gagggtcaag ttgtgaagtt ctggaggcca 550

gaggagccca ttgaagtcat caggcctgac atagcagctc tggttagaca 600

agtgatcata aaaaagaaag aggatctatg agaatgccat tgcgtttcta 650

atagaacaga gaaatgtctc catgagggtt tggtctcatt ttaaacattt 700

ttttttgga gacagtgtct cactctgtca cccaggctgg agtgcagtag 750

tgcgttctca gctcattgca acctctgcct ttttaaacat gctattaaat 800

gtggcaatga aggatttttt tttaatgtta tcttgctatt aagtggtaat 850

gaatgttccc aggatgagga tgttacccaa agcaaaaatc aagagtagcc 900

aaagaatcaa catgaaatat attaactact tcctctgacc atactaaaga 950

attcagaata cacagtgacc aatgtgcctc aatatcttat tgttcaactt 1000

gacattttct aggactgtac ttgatgaaaa tgccaacaca ctagaccact 1050

ctttggattc aagagcactg tgtatgactg aaatttctgg aataactgta 1100

aatggttatg ttaatggaat aaaacacaaa tgttgaaaaa tgtaaaatat 1150

atatacatag attcaaatcc ttatatatgt atgcttgttt tgtgtacagg 1200

attttgtttt ttctttttaa gtacaggttc ctagtgtttt actataactg 1250

tcactatgta tgtaactgac atatataaat agtcatttat aaatgaccgt 1300

attataacat ttgaaaaagt cttcatcaaa aaaaaaaaaa aa 1342

<210> 29
<211> 209
<212> PRT
<213> Homo Sapien

<400> 29

Met Glu Pro Leu Ala Ala Tyr Pro Leu Lys Cys Ser Gly Pro Arg
1 5 10 15

Ala Lys Val Phe Ala Val Leu Leu Ser Ile Val Leu Cys Thr Val
20 25 30

Thr Leu Phe Leu Leu Gln Leu Lys Phe Leu Lys Pro Lys Ile Asn
35 40 45

Ser Phe Tyr Ala Phe Glu Val Lys Asp Ala Lys Gly Arg Thr Val
50 55 60

Ser Leu Glu Lys Tyr Lys Gly Lys Val Ser Leu Val Val Asn Val
65 70 75

Ala Ser Asp Cys Gln Leu Thr Asp Arg Asn Tyr Leu Gly Leu Lys
80 85 90

Glu Leu His Lys Glu Phe Gly Pro Ser His Phe Ser Val Leu Ala
95 100 105

Phe Pro Cys Asn Gln Phe Gly Glu Ser Glu Pro Arg Pro Ser Lys
110 115 120

Glu Val Glu Ser Phe Ala Arg Lys Asn Tyr Gly Val Thr Phe Pro
125 130 135

Ile Phe His Lys Ile Lys Ile Leu Gly Ser Glu Gly Glu Pro Ala
140 145 150

Phe Arg Phe Leu Val Asp Ser Ser Lys Lys Glu Pro Arg Trp Asn
155 160 165

Phe Trp Lys Tyr Leu Val Asn Pro Glu Gly Gln Val Val Lys Phe
170 175 180

Trp Arg Pro Glu Glu Pro Ile Glu Val Ile Arg Pro Asp Ile Ala
185 190 195

Ala Leu Val Arg Gln Val Ile Ile Lys Lys Lys Glu Asp Leu
200 205

<210> 30
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 30
atcctccaac atggagcctc ttgc 24

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
gtatcttgtc aaccctgagg 20

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
taaccagagc tgctatgtca ggcc 24

<210> 33

<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
aggcaaagtt tcactagttg taaacgtggc cagtgactgc caactcacag 50

<210> 34
<211> 3721
<212> DNA
<213> Homo Sapien

<400> 34
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ggccctcctg cttctgctgc tgctactggg gggcgcccac ggcctctttc 100

ctgaggagcc gccgccgctt agcgtggccc ccagggacta cctgaaccac 150

tatcccgtgt ttgtgggcag cgggcccgga cgcctgaccc ccgcagaagg 200

tgctgacgac ctcaacatcc agcgagtcct gcgggtcaac aggacgctgt 250

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gcagcccgtc ggagacaaca tcagcggtat ggcccgctgc ccgtacgacc 550

ccaagcacgc caatgttgcc ctcttctctg acgggatgct cttcacagct 600

actgttaccg acttcctagc cattgatgct gtcatctacc gcagcctcgg 650

ggacaggccc accctgcgca ccgtgaaaca tgactccaag tggttcaaag 700

agccttactt tgtccatgcg gtggagtggg gcagccatgt ctacttcttc 750

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cccggagact cccatttcta cttcaacgtg ctgcaggctg tcacgggcgt 950

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gggggcgga caggactgcg ccccccgtgc cctaggccgg gggcccccg 2700

atgccttggc agtgccagcc acgggaacca ggagcgagag acggtgccag 2750

aacgccgggg cccggggcaa ctccgagtgg gtgctcaagt ccccccgcg 2800

acccacccgc ggagtggggg gccccctccg ccacaaggaa gcacaaccag 2850

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aggttttggt tttttttgc agttttggtt tcttttgcgg ttttctaacc 3000

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cctggaaagg tccctcccca acccaggccc ctggcgtgtg tgggtgtgcg 3150

tgcgtgtgcg tgccgtgttc gtgtgcaagg ggccggggag gtgggcgtgt 3200

gtgtgcgtgc cagcgaaggc tgctgtgggc gtgtgtgtca agtgggccac 3250

gcgtgcaggg tgtgtgtcca cgagcgacga tcgtggtggc cccagcggcc 3300

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cgaggtgccg gttaggagtt tgaacccccc ccactctgca gagggaagcg 3400

gggacaatgc cggggtttca ggcaggagac acgaggaggg cctgcccgga 3450

agtcacatcg gcagcagctg tctaaagggc ttgggggcct ggggggcggc 3500

gaaggtgggt ggggcccctc tgtaaatacg gccccagggt ggtgagagag 3550

tcccatgcca cccgtcccct tgtgacctcc cccctatgac ctccagctga 3600

ccatgcatgc cacgtggctg gctgggtcct ctgccctctt tggagtttgc 3650

ctccccagc cccctcccca tcaataaaac tctgtttaca accaaaaaaa 3700

aaaaaaaaaa aaaaaaaaaa a 3721

<210> 35
<211> 888
<212> PRT
<213> Homo Sapien

<400> 35
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1 5 10 15

Leu Leu Leu Leu Leu Gly Gly Ala His Gly Leu Phe Pro Glu Glu
20 25 30

Pro Pro Pro Leu Ser Val Ala Pro Arg Asp Tyr Leu Asn His Tyr
35 40 45

Pro Val Phe Val Gly Ser Gly Pro Gly Arg Leu Thr Pro Ala Glu
50 55 60

Gly Ala Asp Asp Leu Asn Ile Gln Arg Val Leu Arg Val Asn Arg
65 70 75

Thr Leu Phe Ile Gly Asp Arg Asp Asn Leu Tyr Arg Val Glu Leu
80 85 90

Glu Pro Pro Thr Ser Thr Glu Leu Arg Tyr Gln Arg Lys Leu Thr
95 100 105

Trp Arg Ser Asn Pro Ser Asp Ile Asn Val Cys Arg Met Lys Gly
110 115 120

Lys Gln Glu Gly Glu Cys Arg Asn Phe Val Lys Val Leu Leu Leu
125 130 135

Arg Asp Glu Ser Thr Leu Phe Val Cys Gly Ser Asn Ala Phe Asn
140 145 150

Pro Val Cys Ala Asn Tyr Ser Ile Asp Thr Leu Gln Pro Val Gly
155 160 165

Asp Asn Ile Ser Gly Met Ala Arg Cys Pro Tyr Asp Pro Lys His
170 175 180

Ala Asn Val Ala Leu Phe Ser Asp Gly Met Leu Phe Thr Ala Thr
185 190 195

Val Thr Asp Phe Leu Ala Ile Asp Ala Val Ile Tyr Arg Ser Leu
200 205 210

Gly Asp Arg Pro Thr Leu Arg Thr Val Lys His Asp Ser Lys Trp
215 220 225

Phe Lys Glu Pro Tyr Phe Val His Ala Val Glu Trp Gly Ser His
230 235 240

Val Tyr Phe Phe Phe Arg Glu Ile Ala Met Glu Phe Asn Tyr Leu
245 250 255

Glu Lys Val Val Val Ser Arg Val Ala Arg Val Cys Lys Asn Asp
260 265 270

Val Gly Gly Ser Pro Arg Val Leu Glu Lys Gln Trp Thr Ser Phe
275 280 285

Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp Ser His Phe
290 295 300

Tyr Phe Asn Val Leu Gln Ala Val Thr Gly Val Val Ser Leu Gly

305 310 315

Gly Arg Pro Val Val Leu Ala Val Phe Ser Thr Pro Ser Asn Ser
320 325 330

Ile Pro Gly Ser Ala Val Cys Ala Phe Asp Leu Thr Gln Val Ala
335 340 345

Ala Val Phe Glu Gly Arg Phe Arg Glu Gln Lys Ser Pro Glu Ser
350 355 360

Ile Trp Thr Pro Val Pro Glu Asp Gln Val Pro Arg Pro Arg Pro
365 370 375

Gly Cys Cys Ala Ala Pro Gly Met Gln Tyr Asn Ala Ser Ser Ala
380 385 390

Leu Pro Asp Asp Ile Leu Asn Phe Val Lys Thr His Pro Leu Met
395 400 405

Asp Glu Ala Val Pro Ser Leu Gly His Ala Pro Trp Ile Leu Arg
410 415 420

Thr Leu Met Arg His Gln Leu Thr Arg Val Ala Val Asp Val Gly
425 430 435

Ala Gly Pro Trp Gly Asn Gln Thr Val Val Phe Leu Gly Ser Glu
440 445 450

Ala Gly Thr Val Leu Lys Phe Leu Val Arg Pro Asn Ala Ser Thr
455 460 465

Ser Gly Thr Ser Gly Leu Ser Val Phe Leu Glu Glu Phe Glu Thr
470 475 480

Tyr Arg Pro Asp Arg Cys Gly Arg Pro Gly Gly Gly Glu Thr Gly
485 490 495

Gln Arg Leu Leu Ser Leu Glu Leu Asp Ala Ala Ser Gly Gly Leu
500 505 510

Leu Ala Ala Phe Pro Arg Cys Val Val Arg Val Pro Val Ala Arg
515 520 525

Cys Gln Gln Tyr Ser Gly Cys Met Lys Asn Cys Ile Gly Ser Gln
530 535 540

Asp Pro Tyr Cys Gly Trp Ala Pro Asp Gly Ser Cys Ile Phe Leu
545 550 555

Ser Pro Gly Thr Arg Ala Ala Phe Glu Gln Asp Val Ser Gly Ala
560 565 570

Ser Thr Ser Gly Leu Gly Asp Cys Thr Gly Leu Leu Arg Ala Ser
575 580 585

Leu Ser Glu Asp Arg Ala Gly Leu Val Ser Val Asn Leu Leu Val
590 595 600

Thr Ser Ser Val Ala Ala Phe Val Val Gly Ala Val Val Ser Gly
605 610 615

Phe Ser Val Gly Trp Phe Val Gly Leu Arg Glu Arg Arg Glu Leu
620 625 630

Ala Arg Arg Lys Asp Lys Glu Ala Ile Leu Ala His Gly Ala Gly
635 640 645

Glu Ala Val Leu Ser Val Ser Arg Leu Gly Glu Arg Arg Ala Gln
650 655 660

Gly Pro Gly Gly Arg Gly Gly Gly Gly Gly Gly Gly Ala Gly Val
665 670 675

Pro Pro Glu Ala Leu Leu Ala Pro Leu Met Gln Asn Gly Trp Ala
680 685 690

Lys Ala Thr Leu Leu Gln Gly Gly Pro His Asp Leu Asp Ser Gly
695 700 705

Leu Leu Pro Thr Pro Glu Gln Thr Pro Leu Pro Gln Lys Arg Leu
710 715 720

Pro Thr Pro His Pro His Pro His Ala Leu Gly Pro Arg Ala Trp
725 730 735

Asp His Gly His Pro Leu Leu Pro Ala Ser Ala Ser Ser Ser Leu
740 745 750

Leu Leu Leu Ala Pro Ala Arg Ala Pro Glu Gln Pro Pro Ala Pro
755 760 765

Gly Glu Pro Thr Pro Asp Gly Arg Leu Tyr Ala Ala Arg Pro Gly
770 775 780

Arg Ala Ser His Gly Asp Phe Pro Leu Thr Pro His Ala Ser Pro
785 790 795

Asp Arg Arg Arg Val Val Ser Ala Pro Thr Gly Pro Leu Asp Pro
800 805 810

Ala Ser Ala Ala Asp Gly Leu Pro Arg Pro Trp Ser Pro Pro Pro
815 820 825

Thr Gly Ser Leu Arg Arg Pro Leu Gly Pro His Ala Pro Pro Ala
830 835 840

Ala Thr Leu Arg Arg Thr His Thr Phe Asn Ser Gly Glu Ala Arg
845 850 855

Pro Gly Asp Arg His Arg Gly Cys His Ala Arg Pro Gly Thr Asp
860 865 870

Leu Ala His Leu Leu Pro Tyr Gly Gly Ala Asp Arg Thr Ala Pro
875 880 885

Pro Val Pro

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 36
gaggacctac cggccggaca g 21

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 37
atacaccccg agtactgctg gcag 24

<210> 38
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 38
agacagggca gcggctgctg agcttggagc tggacgcagc tt 42

<210> 39
<211> 2014
<212> DNA
<213> Homo Sapien

<400> 39
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ggccgggaca gcagaacgcc aggggaccct cacctgggcg cgccggggca 100

cgggctttga ttgtcctggg gtcgcggaga cccgcgcgcc tgccctgcac 150

gccgggcggc aacctttgca gtcgcgttgg ctgctgcgat cggccggcgg 200

gtccctgccg aaggctcggc tgcttctgtc cacctcttac acttcttcat 250

ttatcggtgg atcatttcga gagtccgtct tgtaaatgtt tggcactttg 300

ctactttatt gcttctttct ggcgacagtt ccagcactcg ccgagaccgg 350

cggagaaagg cagctgagcc cggagaagag cgaaatatgg ggacccgggc 400

taaaagcaga cgtcgtcctt cccgcccgct atttctatat tcaggcagtg 450

gatacatcag ggaataaatt cacatcttct ccaggcgaaa aggtcttcca 500

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agctacaaaa atctgaaggt ggaaattaaa ttccaagggc aacatgtggc 650

caaatcccca tatattttaa aagggccggt ttaccatgag aactgtgact 700

gtcctctgca agatagtgca gcctggctac gggagatgaa ctgccctgaa 750

accattgctc agattcagag agatctggca catttccctg ctgtggatcc 800

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tggtgtggct ccacagattc caaggatatc gtgatgccta cgtacgattt 1100

gactgattct gttctggaaa ccatgggccg ggtaagtctg gatatgatgt 1150

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cagtagaaaa cacccagaac tcatagacgc tgctttcacc aacttttttct 1300

tctttaaaca cgatgaaaac ctgtatggtc ccattgtgaa acatatttca 1350

ttttttgatt tcttcaagca taagtatcaa ataaatatcg atggcactgt 1400

agcagcttat cgcctgccat atttgctagt tggtgacagt gttgtgctga 1450

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aaacactaca ttccagttaa gagcaacctg agcgatctgc tagaaaaact 1550

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tatttcaaac ttttccagga atatgccaat ttacaagtga gtgagcccca 1700

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aaataacttc tattagaata atggtgctct gaagactctt cttaactaaa 1850

aagaagaatt tttttaagta ttaattccat ggacaatata aaatctgtgt 1900

gattgtttgc agtatgaaga cacatttcta cttatgcagt attctcatga 1950

ctgtacttta aagtacattt ttagaatttt ataataaaac cacctttatt 2000

ttaaaggaaa aaaa 2014

<210> 40
<211> 502
<212> PRT
<213> Homo Sapien

<400> 40

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                20                  25                  30

Lys Ser Glu Ile Trp Gly Pro Gly Leu Lys Ala Asp Val Val Leu
                35                  40                  45

Pro Ala Arg Tyr Phe Tyr Ile Gln Ala Val Asp Thr Ser Gly Asn
                50                  55                  60

Lys Phe Thr Ser Ser Pro Gly Glu Lys Val Phe Gln Val Lys Val
                65                  70                  75

Ser Ala Pro Glu Glu Gln Phe Thr Arg Val Gly Val Gln Val Leu
                80                  85                  90

Asp Arg Lys Asp Gly Ser Phe Ile Val Arg Tyr Arg Met Tyr Ala
                95                 100                 105

Ser Tyr Lys Asn Leu Lys Val Glu Ile Lys Phe Gln Gly Gln His
               110                 115                 120

Val Ala Lys Ser Pro Tyr Ile Leu Lys Gly Pro Val Tyr His Glu
               125                 130                 135

Asn Cys Asp Cys Pro Leu Gln Asp Ser Ala Ala Trp Leu Arg Glu
               140                 145                 150

Met Asn Cys Pro Glu Thr Ile Ala Gln Ile Gln Arg Asp Leu Ala
               155                 160                 165

His Phe Pro Ala Val Asp Pro Glu Lys Ile Ala Val Glu Ile Pro
               170                 175                 180

Lys Arg Phe Gly Gln Arg Gln Ser Leu Cys His Tyr Thr Leu Lys
               185                 190                 195

Asp Asn Lys Val Tyr Ile Lys Thr His Gly Glu His Val Gly Phe
               200                 205                 210

Arg Ile Phe Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys Val
               215                 220                 225

Lys Met Pro Asp Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro
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230 235 240

Leu Glu Lys Lys Lys Ser Asn Ser Asn Ile His Pro Ile Phe Ser
245 250 255

Trp Cys Gly Ser Thr Asp Ser Lys Asp Ile Val Met Pro Thr Tyr
260 265 270

Asp Leu Thr Asp Ser Val Leu Glu Thr Met Gly Arg Val Ser Leu
275 280 285

Asp Met Met Ser Val Gln Ala Asn Thr Gly Pro Pro Trp Glu Ser
290 295 300

Lys Asn Ser Thr Ala Val Trp Arg Gly Arg Asp Ser Arg Lys Glu
305 310 315

Arg Leu Glu Leu Val Lys Leu Ser Arg Lys His Pro Glu Leu Ile
320 325 330

Asp Ala Ala Phe Thr Asn Phe Phe Phe Phe Lys His Asp Glu Asn
335 340 345

Leu Tyr Gly Pro Ile Val Lys His Ile Ser Phe Phe Asp Phe Phe
350 355 360

Lys His Lys Tyr Gln Ile Asn Ile Asp Gly Thr Val Ala Ala Tyr
365 370 375

Arg Leu Pro Tyr Leu Leu Val Gly Asp Ser Val Val Leu Lys Gln
380 385 390

Asp Ser Ile Tyr Tyr Glu His Phe Tyr Asn Glu Leu Gln Pro Trp
395 400 405

Lys His Tyr Ile Pro Val Lys Ser Asn Leu Ser Asp Leu Leu Glu
410 415 420

Lys Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala Lys Lys Ile
425 430 435

Ala Lys Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met Gly Asp
440 445 450

Asp Ile Phe Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala Asn
455 460 465

Leu Gln Val Ser Glu Pro Gln Ile Arg Glu Gly Met Lys Arg Val
470 475 480

Glu Pro Gln Thr Glu Asp Asp Leu Phe Pro Cys Thr Cys His Arg
485 490 495

Lys Lys Thr Lys Asp Glu Leu
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<210> 41
<211> 26

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
gaaggtggaa attaaattcc aagggc 26

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
cgataagctg ctacagtgcc atcg 24

<210> 43
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
gtgactgtcc tctgcaagat agtgcagcct ggctacggga 40

<210> 44
<211> 2395
<212> DNA
<213> Homo Sapien

<400> 44
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cggggattct tcccggctcc cgttcgttcc tctgccagag cggaacacgg 200

agcggagccc ccagcgcccg aaccctcggc tggagccagt tctaactgga 250

ccacgctgcc accacctctc ttcagtaaag ttgttattgt tctgatagat 300

gccttgagag atgattttgt gtttgggtca aagggtgtga aatttatgcc 350

ctacacaact taccttgtgg aaaaaggagc atctcacagt tttgtggctg 400

aagcaaagcc acctacagtt actatgcctc gaatcaaggc attgatgacg 450

gggagccttc ctggctttgt cgacgtcatc aggaacctca attctcctgc 500

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tagtctttta tggagatgaa acctgggtta aattattccc aaagcatttt 600

gtggaatatg atggaacaac ctcatttttc gtgtcagatt acacagaggt 650

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gggacatatt aatcctccac tacctggggc tggaccacat tggccacatt 750

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ctgcagctga gggaagaaga gacaatcggc ctggacactc aggagggtca 1900

aaaggagact tggtcgcacc actcatcctg ccacccccag aatgcatcct 1950

gcctcatcag gtccagattt ctttccaagg cggacgtttt ctgttggaat 2000

tcttagtcct tggcctcgga caccttcatt cgttagctgg ggagtggtgg 2050

tgaggcagtg aagaagaggc ggatggtcac actcagatcc acagagccca 2100

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aaccctgcac agccctcatc ccctcttggc ttgagccgtc agaggccctg 2200

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gggctcatgc tctctctcct gctattgaat tagtacctag ctgcacacag 2350

tatgtagtta ccaaaagaat aaacggcaat aattgagaaa aaaaa 2395

<210> 45
<211> 310
<212> PRT
<213> Homo Sapien

<400> 45

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Glu	Val	Leu	Gly	Ile	Ala	Val	Phe	Leu	Arg	Gly	Phe	Phe	Pro	Ala
				20				25						30
Pro	Val	Arg	Ser	Ser	Ala	Arg	Ala	Glu	His	Gly	Ala	Glu	Pro	Pro
				35				40						45
Ala	Pro	Glu	Pro	Ser	Ala	Gly	Ala	Ser	Ser	Asn	Trp	Thr	Thr	Leu
				50				55						60
Pro	Pro	Pro	Leu	Phe	Ser	Lys	Val	Val	Ile	Val	Leu	Ile	Asp	Ala
				65				70						75
Leu	Arg	Asp	Asp	Phe	Val	Phe	Gly	Ser	Lys	Gly	Val	Lys	Phe	Met
				80				85						90
Pro	Tyr	Thr	Thr	Tyr	Leu	Val	Glu	Lys	Gly	Ala	Ser	His	Ser	Phe
				95				100						105
Val	Ala	Glu	Ala	Lys	Pro	Pro	Thr	Val	Thr	Met	Pro	Arg	Ile	Lys
				110				115						120
Ala	Leu	Met	Thr	Gly	Ser	Leu	Pro	Gly	Phe	Val	Asp	Val	Ile	Arg
				125				130						135
Asn	Leu	Asn	Ser	Pro	Ala	Leu	Leu	Glu	Asp	Ser	Val	Ile	Arg	Gln
				140				145						150
Ala	Lys	Ala	Ala	Gly	Lys	Arg	Ile	Val	Phe	Tyr	Gly	Asp	Glu	Thr
				155				160						165
Trp	Val	Lys	Leu	Phe	Pro	Lys	His	Phe	Val	Glu	Tyr	Asp	Gly	Thr
				170				175						180

Thr Ser Phe Phe Val Ser Asp Tyr Thr Glu Val Asp Asn Asn Val
185 190 195

Thr Arg His Leu Asp Lys Val Leu Lys Arg Gly Asp Trp Asp Ile
200 205 210

Leu Ile Leu His Tyr Leu Gly Leu Asp His Ile Gly His Ile Ser
215 220 225

Gly Pro Asn Ser Pro Leu Ile Gly Gln Lys Leu Ser Glu Met Asp
230 235 240

Ser Val Leu Met Lys Ile His Thr Ser Leu Gln Ser Lys Glu Arg
245 250 255

Glu Thr Pro Leu Pro Asn Leu Leu Val Leu Cys Gly Asp His Gly
260 265 270

Met Ser Glu Thr Gly Ser His Gly Ala Ser Ser Thr Glu Glu Val
275 280 285

Asn Thr Pro Leu Ile Leu Ile Ser Ser Ala Phe Glu Arg Lys Pro
290 295 300

Gly Asp Ile Arg His Pro Lys His Val Gln
305 310

<210> 46
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 46
cgggactttc gctacctgtt gc 22

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
catcatattc cacaaaatgc tttggg 26

<210> 48
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48

ccttcgggga ttcttcccgg ctcccgttcg ttcctctg 38

<210> 49
<211> 918
<212> DNA
<213> Homo Sapien

<400> 49
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agcaatggca atgggggtcc ccagagtcat tctgctctgc ctctttgggg 100

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cacacctact ttggcccctt tgacctcagg gccatgaagc tgcccagcat 200

ctcctgtcct catgagtgct ttgaggctat cctgtctctg gacaccgggt 250

atcgcgcgcc ggtgaccctg gtgcggaagg gctgctggac cgggcctcct 300

gcgggccaga cgcaatcgaa cccggacgcg ctgccgccag actactcggt 350

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gccgagtgct acgcctgtat cggggtccac caggatgact gcgctatcgg 500

caggtcccga cgagtccagt gtcaccagga ccagaccgcc tgcttccagg 550

gcagtggcag aatgacagtt ggcaatttct cagtccctgt gtacatcaga 600

acctgccacc ggccctcctg caccaccgag ggcaccacca gcccctggac 650

agccatcgac ctccagggct cctgctgtga ggggtacctc tgcaacagga 700

aatccatgac ccagcccttc accagtgctt cagccaccac ccctccccga 750

gcactacagg tcctggccct gctcctccca gtcctcctgc tggtggggct 800

ctcagcatag accgcccctc caggatgctg gggacagggc tcacacacct 850

cattcttgct gcttcagccc ctatcacata gctcactgga aaatgatgtt 900

aaagtaagaa ttgcaaaa 918

<210> 50
<211> 251
<212> PRT
<213> Homo Sapien

<400> 50
Met Ala Met Gly Val Pro Arg Val Ile Leu Leu Cys Leu Phe Gly
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Ala Ala Leu Cys Leu Thr Gly Ser Gln Ala Leu Gln Cys Tyr Ser
20 25 30

Phe Glu His Thr Tyr Phe Gly Pro Phe Asp Leu Arg Ala Met Lys
35 40 45

Leu Pro Ser Ile Ser Cys Pro His Glu Cys Phe Glu Ala Ile Leu
50 55 60

Ser Leu Asp Thr Gly Tyr Arg Ala Pro Val Thr Leu Val Arg Lys
65 70 75

Gly Cys Trp Thr Gly Pro Pro Ala Gly Gln Thr Gln Ser Asn Pro
80 85 90

Asp Ala Leu Pro Pro Asp Tyr Ser Val Val Arg Gly Cys Thr Thr
95 100 105

Asp Lys Cys Asn Ala His Leu Met Thr His Asp Ala Leu Pro Asn
110 115 120

Leu Ser Gln Ala Pro Asp Pro Pro Thr Leu Ser Gly Ala Glu Cys
125 130 135

Tyr Ala Cys Ile Gly Val His Gln Asp Asp Cys Ala Ile Gly Arg
140 145 150

Ser Arg Arg Val Gln Cys His Gln Asp Gln Thr Ala Cys Phe Gln
155 160 165

Gly Ser Gly Arg Met Thr Val Gly Asn Phe Ser Val Pro Val Tyr
170 175 180

Ile Arg Thr Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr
185 190 195

Ser Pro Trp Thr Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly
200 205 210

Tyr Leu Cys Asn Arg Lys Ser Met Thr Gln Pro Phe Thr Ser Ala
215 220 225

Ser Ala Thr Thr Pro Pro Arg Ala Leu Gln Val Leu Ala Leu Leu
230 235 240

Leu Pro Val Leu Leu Leu Val Gly Leu Ser Ala
245 250

<210> 51
<211> 3288
<212> DNA
<213> Homo Sapien

<400> 51
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gattgggaaa gggaaaggac aaaaaagacc cctgggctac acggcgtagg 100

tgcagggttt cctactgctg ttcttttatg ctgggagctg tggctgtaac 150

caactaggaa ataacgtatg cagcagctat ggctgtcaga gagttgtgct 200

tcccaagaca aaggcaagtc ctgtttcttt ttctttttg gggagtgtcc 250

ttggcaggtt ctgggtttgg acgttattcg gtgactgagg aaacagagaa 300

aggatccttt gtggtcaatc tggcaaagga tctgggacta gcagaggggg 350

agctggctgc aaggggaacc agggtggttt ccgatgataa caaacaatac 400

ctgctcctgg attcacatac cgggaatttg ctcacaaatg agaaactgga 450

ccgagagaag ctgtgtggcc ctaaagagcc ctgtatgctg tatttccaaa 500

ttttaatgga tgatcccttt cagatttacc gggctgagct gagagtcagg 550

gatataaatg atcacgcgcc agtatttcag gacaaagaaa cagtcttaaa 600

aatatcagaa aatacagctg aagggacagc atttagacta gaaagagcac 650

aggatccaga tggaggactt aacggtatcc aaaactacac gatcagcccc 700

aactcttttt tccatattaa cattagtggc ggtgatgaag gcatgatata 750

tccagagcta gtgttggaca aagcactgga tcgggaggag cagggagagc 800

tcagcttaac cctcacagcg ctggatggtg ggtctccatc caggtctggg 850

acctctactg tacgcatcgt tgtcttggac gtcaatgaca atgccccaca 900

gtttgcccag gctctgtatg agacccaggc tccagaaaac agccccattg 950

ggttccttat tgttaaggta tgggcagaag atgtagactc tggagtcaac 1000

gcggaagtat cctattcatt ttttgatgcc tcagaaaata ttcgaacgac 1050

ctttcaaatc aatccttttt ctggggaaat ctttctcaga gaattgcttg 1100

attatgagtt agtaaattct tacaaaataa atatacaggc aatggacggt 1150

ggaggccttt ctgcaagatg tagggtttta gtggaagtat tggacaccaa 1200

tgacaatccc cctgaactga tcgtatcatc attttccaac tctgttgctg 1250

agaattctcc tgagacgccg ctggctgttt ttaagattaa tgacagagac 1300

tctggagaaa atggaaagat ggtttgctac attcaagaga atctgccatt 1350

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cgctggacag agagatcaga gccgagtaca acatcactat caccgtcact 1450

gacttgggga cacccaggct gaaaaccgag cacaacataa cggtcctggt 1500

ctccgacgtc aatgacaacg cccccgcctt cacccaaacc tcctacaccc 1550

tgttcgtccg cgagaacaac agccccgccc tgcacatcgg cagcgtcagc 1600

gccacagaca gagactcggg caccaacgcc caggtcacct actcgctgct 1650

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gagcagagag gcgctggtgc gcgtgctggt gctggacgcc aacgacaact 1850

cgcccttcgt gctgtacccg ctgcagaacg gctccgcgcc ctgcaccgag 1900

ctggtgcccc gggcggccga gccgggctac ctggtgacca aggtggtggc 1950

ggtggacggc gactcgggcc agaacgcctg gctgtcgtac cagctgctca 2000

aggccacgga gcccgggctg ttcggtgtgt gggcgcacaa tggggaggtg 2050

cgcaccgcca ggctgctgag cgagcgcgac gcagccaagc acaggctcgt 2100

ggtgcttgtc aaggacaatg gcgagcctcc tcgctcggcc accgccacgc 2150

tgcacttgct cctggtggac ggcttctccc agccctacct gcctctcccg 2200

gaggcggccc cggcccaggc ccaggccgag gccgacttgc tcaccgtcta 2250

cctggtggtg gcgttggcct cggtgtcttc gctcttcctc ctctcggtgc 2300

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gatattcagg cacagggccc tgggaggaag ggtgaagaaa attccacctt 2550

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cccctgtggt tttacaatgt ttcatcattt ttttgcatta ataacaactg 2750

ggtttaattt aatgagtatt tttttctaaa tgatagtgtt aaggttttaa 2800

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atctgaggtt ttgattcatt tcagagcttg catctcatga ttctaatcac 2900

ttctgtctat agtgtacttg ctctatttaa gaaggcatat ctacatttcc 2950

aaactcattc taacattcta tatattcgtg tttgaaaacc atgtcattta 3000

tttctacatc atgtatttaa aaagaaatat ttctctacta ctatgctcat 3050

gacaaaatga aacaaagcat attgtgagca atactgaaca tcaataatac 3100

ccttagttta tatacttatt attttatctt taagcatgct acttttactt 3150

ggccaatatt ttcttatgtt aacttttgct gatgtataaa acagactatg 3200

ccttataatt gaaataaaat tataatctgc ctgaaaatga ataaaaataa 3250

aacattttga aatgtgaaaa aaaaaaaaaa aaaaaaaa 3288

<210> 52
<211> 800
<212> PRT
<213> Homo Sapien

<400> 52

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Phe	Leu	Phe	Leu	Phe	Trp	Gly	Val	Ser	Leu	Ala	Gly	Ser	Gly	Phe	
				20				25						30	
Gly	Arg	Tyr	Ser	Val	Thr	Glu	Glu	Thr	Glu	Lys	Gly	Ser	Phe	Val	
				35				40						45	
Val	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Ala	Glu	Gly	Glu	Leu	Ala	
				50				55						60	
Ala	Arg	Gly	Thr	Arg	Val	Val	Ser	Asp	Asp	Asn	Lys	Gln	Tyr	Leu	
				65				70						75	
Leu	Leu	Asp	Ser	His	Thr	Gly	Asn	Leu	Leu	Thr	Asn	Glu	Lys	Leu	
				80				85						90	
Asp	Arg	Glu	Lys	Leu	Cys	Gly	Pro	Lys	Glu	Pro	Cys	Met	Leu	Tyr	
				95				100						105	
Phe	Gln	Ile	Leu	Met	Asp	Asp	Pro	Phe	Gln	Ile	Tyr	Arg	Ala	Glu	
				110				115						120	
Leu	Arg	Val	Arg	Asp	Ile	Asn	Asp	His	Ala	Pro	Val	Phe	Gln	Asp	
				125				130						135	
Lys	Glu	Thr	Val	Leu	Lys	Ile	Ser	Glu	Asn	Thr	Ala	Glu	Gly	Thr	
				140				145						150	
Ala	Phe	Arg	Leu	Glu	Arg	Ala	Gln	Asp	Pro	Asp	Gly	Gly	Leu	Asn	
				155				160						165	
Gly	Ile	Gln	Asn	Tyr	Thr	Ile	Ser	Pro	Asn	Ser	Phe	Phe	His	Ile	
				170				175						180	
Asn	Ile	Ser	Gly	Gly	Asp	Glu	Gly	Met	Ile	Tyr	Pro	Glu	Leu	Val	
				185				190						195	
Leu	Asp	Lys	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Gly	Glu	Leu	Ser	Leu	
				200				205						210	
Thr	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Ser	Pro	Ser	Arg	Ser	Gly	Thr	
				215				220						225	

Ser Thr Val Arg Ile Val Val Leu Asp Val Asn Asp Asn Ala Pro
230 235 240

Gln Phe Ala Gln Ala Leu Tyr Glu Thr Gln Ala Pro Glu Asn Ser
245 250 255

Pro Ile Gly Phe Leu Ile Val Lys Val Trp Ala Glu Asp Val Asp
260 265 270

Ser Gly Val Asn Ala Glu Val Ser Tyr Ser Phe Phe Asp Ala Ser
275 280 285

Glu Asn Ile Arg Thr Thr Phe Gln Ile Asn Pro Phe Ser Gly Glu
290 295 300

Ile Phe Leu Arg Glu Leu Leu Asp Tyr Glu Leu Val Asn Ser Tyr
305 310 315

Lys Ile Asn Ile Gln Ala Met Asp Gly Gly Gly Leu Ser Ala Arg
320 325 330

Cys Arg Val Leu Val Glu Val Leu Asp Thr Asn Asp Asn Pro Pro
335 340 345

Glu Leu Ile Val Ser Ser Phe Ser Asn Ser Val Ala Glu Asn Ser
350 355 360

Pro Glu Thr Pro Leu Ala Val Phe Lys Ile Asn Asp Arg Asp Ser
365 370 375

Gly Glu Asn Gly Lys Met Val Cys Tyr Ile Gln Glu Asn Leu Pro
380 385 390

Phe Leu Leu Lys Pro Ser Val Glu Asn Phe Tyr Ile Leu Ile Thr
395 400 405

Glu Gly Ala Leu Asp Arg Glu Ile Arg Ala Glu Tyr Asn Ile Thr
410 415 420

Ile Thr Val Thr Asp Leu Gly Thr Pro Arg Leu Lys Thr Glu His
425 430 435

Asn Ile Thr Val Leu Val Ser Asp Val Asn Asp Asn Ala Pro Ala
440 445 450

Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser
455 460 465

Pro Ala Leu His Ile Gly Ser Val Ser Ala Thr Asp Arg Asp Ser
470 475 480

Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp
485 490 495

Pro His Leu Pro Leu Ala Ser Leu Val Ser Ile Asn Ala Asp Asn
500 505 510

Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln

515 520 525

Ala Phe Glu Phe Arg Val Gly Ala Thr Asp Arg Gly Ser Pro Ala
530 535 540

Leu Ser Arg Glu Ala Leu Val Arg Val Leu Val Leu Asp Ala Asn
545 550 555

Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala
560 565 570

Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu
575 580 585

Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala
590 595 600

Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Pro Gly Leu Phe
605 610 615

Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu
620 625 630

Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys
635 640 645

Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Leu
650 655 660

Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu
665 670 675

Ala Ala Pro Ala Gln Ala Gln Ala Glu Ala Asp Leu Leu Thr Val
680 685 690

Tyr Leu Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Leu
695 700 705

Ser Val Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg
710 715 720

Ala Ala Ser Val Gly Arg Cys Ser Val Pro Glu Gly Pro Phe Pro
725 730 735

Gly His Leu Val Asp Val Arg Gly Ala Glu Thr Leu Ser Gln Ser
740 745 750

Tyr Gln Tyr Glu Val Cys Leu Thr Gly Gly Pro Gly Thr Ser Glu
755 760 765

Phe Lys Phe Leu Lys Pro Val Ile Ser Asp Ile Gln Ala Gln Gly
770 775 780

Pro Gly Arg Lys Gly Glu Glu Asn Ser Thr Phe Arg Asn Ser Phe
785 790 795

Gly Phe Asn Ile Gln
800

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
ctggggagtg tccttggcag gttc 24

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 54
cagcatacag ggctctttag ggcacac 27

<210> 55
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 55
cggtgactga ggaaacagag aaaggatcct ttgtggtcaa tctggc 46

<210> 56
<211> 2242
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 2181
<223> unknown base

<400> 56
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tataccagcc tcgtcttcct tccgggggac aacgtgggtc agggcacaga 100

gagatattta atgtcaccct cttggggctt tcatgggact ccctctgcca 150

catttttgg aggttgggaa agttgctaga ggcttcagaa ctccagccta 200

atggatccca aactcgggag aatggctgcg tccctgctgg ctgtgctgct 250

gctgctgctg gagcgcggca tgttctcctc accctccccg cccccggcgc 300

tgttagagaa agtcttccag tacattgacc tccatcagga tgaatttgtg 350

cagacgctga aggagtgggt ggccatcgag agcgactctg tccagcctgt 400

gcctcgcttc agacaagagc tcttcagaat gatggccgtg gctgcggaca 450

cgctgcagcg cctgggggcc cgtgtggcct cggtggacat gggtcctcag 500

cagctgcccg atggtcagag tcttccaata cctcccgtca tcctggccga 550

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ctgacggagg tagacgggaa actttatgga cgaggagcga ccgacaacaa 700

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gctggctctg ttgccctgga ggaacttgtg gaaaaagaaa aggaccgatt 850

cttctctggt gtggactaca ttgtaatttc agataacctg tggatcagcc 900

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ccgagttata ggaaaatttt caatccgtct agtccctcac atgaatgtgt 1350

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agaaatagtt ccaacaagat ggttgtttcc atgactctag gactacaccc 1450

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tcagaacagt gtttggaaca gaaccagata tgatccggga tggatccacc 1550

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aattccgctg ggagctgttg atgatggaga acattcgcag aatgagaaaa 1650

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ttagagatgg cccagctcca ttaatcacaa gaaccttcta gtctgatctg 1750

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2242

<210> 57
<211> 507
<212> PRT
<213> Homo Sapien

<400> 57

Met Asp Pro Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val
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Leu Leu Leu Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro
20 25 30

Pro Pro Ala Leu Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His
35 40 45

Gln Asp Glu Phe Val Gln Thr Leu Lys Glu Trp Val Ala Ile Glu
50 55 60

Ser Asp Ser Val Gln Pro Val Pro Arg Phe Arg Gln Glu Leu Phe
65 70 75

Arg Met Met Ala Val Ala Ala Asp Thr Leu Gln Arg Leu Gly Ala
80 85 90

Arg Val Ala Ser Val Asp Met Gly Pro Gln Gln Leu Pro Asp Gly
95 100 105

Gln Ser Leu Pro Ile Pro Pro Val Ile Leu Ala Glu Leu Gly Ser
110 115 120

Asp Pro Thr Lys Gly Thr Val Cys Phe Tyr Gly His Leu Asp Val
125 130 135

Gln Pro Ala Asp Arg Gly Asp Gly Trp Leu Thr Asp Pro Tyr Val
140 145 150

Leu Thr Glu Val Asp Gly Lys Leu Tyr Gly Arg Gly Ala Thr Asp
155 160 165

Asn Lys Gly Pro Val Leu Ala Trp Ile Asn Ala Val Ser Ala Phe

170 175 180

Arg Ala Leu Glu Gln Asp Leu Pro Val Asn Ile Lys Phe Ile Ile
185 190 195

Glu Gly Met Glu Glu Ala Gly Ser Val Ala Leu Glu Glu Leu Val
200 205 210

Glu Lys Glu Lys Asp Arg Phe Phe Ser Gly Val Asp Tyr Ile Val
215 220 225

Ile Ser Asp Asn Leu Trp Ile Ser Gln Arg Lys Pro Ala Ile Thr
230 235 240

Tyr Gly Thr Arg Gly Asn Ser Tyr Phe Met Val Glu Val Lys Cys
245 250 255

Arg Asp Gln Asp Phe His Ser Gly Thr Phe Gly Gly Ile Leu His
260 265 270

Glu Pro Met Ala Asp Leu Val Ala Leu Leu Gly Ser Leu Val Asp
275 280 285

Ser Ser Gly His Ile Leu Val Pro Gly Ile Tyr Asp Glu Val Val
290 295 300

Pro Leu Thr Glu Glu Glu Ile Asn Thr Tyr Lys Ala Ile His Leu
305 310 315

Asp Leu Glu Glu Tyr Arg Asn Ser Ser Arg Val Glu Lys Phe Leu
320 325 330

Phe Asp Thr Lys Glu Glu Ile Leu Met His Leu Trp Arg Tyr Pro
335 340 345

Ser Leu Ser Ile His Gly Ile Glu Gly Ala Phe Asp Glu Pro Gly
350 355 360

Thr Lys Thr Val Ile Pro Gly Arg Val Ile Gly Lys Phe Ser Ile
365 370 375

Arg Leu Val Pro His Met Asn Val Ser Ala Val Glu Lys Gln Val
380 385 390

Thr Arg His Leu Glu Asp Val Phe Ser Lys Arg Asn Ser Ser Asn
395 400 405

Lys Met Val Val Ser Met Thr Leu Gly Leu His Pro Trp Ile Ala
410 415 420

Asn Ile Asp Asp Thr Gln Tyr Leu Ala Ala Lys Arg Ala Ile Arg
425 430 435

Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr
440 445 450

Ile Pro Ile Ala Lys Met Phe Gln Glu Ile Val His Lys Ser Val
455 460 465

Val Leu Ile Pro Leu Gly Ala Val Asp Asp Gly Glu His Ser Gln
470 475 480

Asn Glu Lys Ile Asn Arg Trp Asn Tyr Ile Glu Gly Thr Lys Leu
485 490 495

Phe Ala Ala Phe Phe Leu Glu Met Ala Gln Leu His
500 505

<210> 58
<211> 1470
<212> DNA
<213> Homo Sapien

<400> 58
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acactacctt cccgaagttg aaggcaagcg gtgattgttt gtagacggcg 100

ctttgtcatg ggacctgtgc ggttgggaat attgcttttc ctttttttgg 150

ccgtgcacga ggcttgggct gggatgttga aggaggagga cgatgacaca 200

gaacgcttgc ccagcaaatg cgaagtgtgt aagctgctga gcacagagct 250

acaggcggaa ctgagtcgca ccggtcgatc tcgagaggtg ctggagctgg 300

ggcaggtgct ggatacaggc aagaggaaga gacacgtgcc ttacagcgtt 350

tcagagacaa ggctggaaga ggccttagag aatttatgtg agcggatcct 400

ggactatagt gttcacgctg agcgcaaggg ctcactgaga tatgccaagg 450

gtcagagtca gaccatggca acactgaaag gcctagtgca gaaggggtg 500

aaggtggatc tggggatccc tctggagctt tgggatgagc ccagcgtgga 550

ggtcacatac ctcaagaagc agtgtgagac catgttggag gagtttgaag 600

acattgtggg agactggtac ttccaccatc aggagcagcc cctacaaaat 650

tttctctgtg aaggtcatgt gctcccagct gctgaaactg catgtctaca 700

ggaaacttgg actggaaagg agatcacaga tggggaagag aaaacagaag 750

gggaggaaga gcaggaggag gaggaggaag aggaggaaga ggaaggggga 800

gacaagatga ccaagacagg aagccacccc aaacttgacc gagaagatct 850

ttgacccttg cctttgagcc cccaggaggg gaagggatca tggagagccc 900

tctaaagcct gcactctccc tgctccacag ctttcagggt gtgtttatga 950

gtgactccac ccaagcttgt agctgttctc tcccatctaa cctcaggcaa 1000

gatcctggtg aaacagcatg acatggcttc tggggtggag ggtgggggtg 1050

gaggtcctgc tcctagagat gaactctatc cagcccctta attggcaggt 1100

gtatgtgctg acagtactga aagctttcct ctttaactga tcccaccccc 1150

acccaaaagt cagcagtggc actggagctg tgggctttgg ggaagtcact 1200

tagctcctta aggtctgttt ttagaccctt ccaaggaaga ggccagaacg 1250

gacattctct gcgatctata tacattgcct gtatccagga ggctacacac 1300

cagcaaaccg tgaaggagaa tgggacactg ggtcatggcc tggagttgct 1350

gataatttag gtgggataga tacttggtct acttaagctc aatgtaaccc 1400

agagcccacc atatagtttt ataggtgctc aactttctat atcgctatta 1450

aacttttttc ttttttttcta 1470

<210> 59
<211> 248
<212> PRT
<213> Homo Sapien

<400> 59

Met	Gly	Pro	Val	Arg	Leu	Gly	Ile	Leu	Leu	Phe	Leu	Phe	Leu	Ala
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Val	His	Glu	Ala	Trp	Ala	Gly	Met	Leu	Lys	Glu	Glu	Asp	Asp	Asp
				20				25						30
Thr	Glu	Arg	Leu	Pro	Ser	Lys	Cys	Glu	Val	Cys	Lys	Leu	Leu	Ser
				35				40						45
Thr	Glu	Leu	Gln	Ala	Glu	Leu	Ser	Arg	Thr	Gly	Arg	Ser	Arg	Glu
				50				55						60
Val	Leu	Glu	Leu	Gly	Gln	Val	Leu	Asp	Thr	Gly	Lys	Arg	Lys	Arg
				65				70						75
His	Val	Pro	Tyr	Ser	Val	Ser	Glu	Thr	Arg	Leu	Glu	Glu	Ala	Leu
				80				85						90
Glu	Asn	Leu	Cys	Glu	Arg	Ile	Leu	Asp	Tyr	Ser	Val	His	Ala	Glu
				95				100						105
Arg	Lys	Gly	Ser	Leu	Arg	Tyr	Ala	Lys	Gly	Gln	Ser	Gln	Thr	Met
				110				115						120
Ala	Thr	Leu	Lys	Gly	Leu	Val	Gln	Lys	Gly	Val	Lys	Val	Asp	Leu
				125				130						135
Gly	Ile	Pro	Leu	Glu	Leu	Trp	Asp	Glu	Pro	Ser	Val	Glu	Val	Thr
				140				145						150
Tyr	Leu	Lys	Lys	Gln	Cys	Glu	Thr	Met	Leu	Glu	Glu	Phe	Glu	Asp
				155				160						165
Ile	Val	Gly	Asp	Trp	Tyr	Phe	His	His	Gln	Glu	Gln	Pro	Leu	Gln
				170				175						180

Asn Phe Leu Cys Glu Gly His Val Leu Pro Ala Ala Glu Thr Ala
185 190 195

Cys Leu Gln Glu Thr Trp Thr Gly Lys Glu Ile Thr Asp Gly Glu
200 205 210

Glu Lys Thr Glu Gly Glu Glu Glu Gln Glu Glu Glu Glu Glu Glu
215 220 225

Glu Glu Glu Glu Gly Gly Asp Lys Met Thr Lys Thr Gly Ser His
230 235 240

Pro Lys Leu Asp Arg Glu Asp Leu
245

<210> 60
<211> 890
<212> DNA
<213> Homo Sapien

<400> 60
aagtacttgt gtccgggtgg tggactggat tagctgcgga gccctggaag 50

ctgcctgtcc ttctccctgt gcttaaccag aggtgcccat gggttggaca 100

atgaggctgg tcacagcagc actgttactg ggtctcatga tggtggtcac 150

tggagacgag gatgagaaca gcccgtgtgc ccatgaggcc ctcttggacg 200

aggacaccct cttttgccag ggccttgaag ttttctaccc agagttgggg 250

aacattggct gcaaggttgt tcctgattgt aacaactaca gacagaagat 300

cacctcctgg atggagccga tagtcaagtt cccgggggcc gtggacggcg 350

caacctatat cctggtgatg gtggatccag atgcccctag cagagcagaa 400

cccagacaga gattctggag acattggctg gtaacagata tcaagggcgc 450

cgacctgaag aaagggaaga ttcagggcca ggagttatca gcctaccagg 500

ctccctcccc accggcacac agtggcttcc atcgctacca gttctttgtc 550

tatcttcagg aaggaaaagt catctctctc cttcccaagg aaaacaaaac 600

tcgaggctct tggaaaatgg acagatttct gaaccgcttc cacctgggcg 650

aacctgaagc aagcacccag ttcatgaccc agaactacca ggactcacca 700

accctccagg ctcccagagg aagggccagc gagcccaagc acaaaaccag 750

gcagagatag ctgcctgcta gatagccggc tttgccatcc gggcatgtgg 800

ccacactgct caccaccgac gatgtgggta tggaaccccc tctggataca 850

gaaccccttc ttttccaaat taaaaaaaaa aatcatcaaa 890

<210> 61

<211> 223
<212> PRT
<213> Homo Sapien

<400> 61
Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly
1 5 10 15

Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys
20 25 30

Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly
35 40 45

Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val
50 55 60

Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met
65 70 75

Glu Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr
80 85 90

Ile Leu Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro
95 100 105

Arg Gln Arg Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly
110 115 120

Ala Asp Leu Lys Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala
125 130 135

Tyr Gln Ala Pro Ser Pro Pro Ala His Ser Gly Phe His Arg Tyr
140 145 150

Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys Val Ile Ser Leu Leu
155 160 165

Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys Met Asp Arg Phe
170 175 180

Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser Thr Gln Phe
185 190 195

Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala Pro Arg
200 205 210

Gly Arg Ala Ser Glu Pro Lys His Lys Thr Arg Gln Arg
215 220

<210> 62
<211> 1321
<212> DNA
<213> Homo Sapien

<400> 62
gtcgacccac gcgtccgaag ctgctggagc cacgattcag tcccctggac 50

tgtagataaa gacccttttct tgccaggtgc tgagacaacc acactatgag 100

aggcactcca ggagacgctg atggtggagg aagggccgtc tatcaatcaa 150

tcactgttgc tgttatcaca tgcaagtatc cagaggctct tgagcaaggc 200

agaggggatc ccatttattt gggaatccag aatccagaaa tgtgtttgta 250

ttgtgagaag gttggagaac agcccacatt gcagctaaaa gagcagaaga 300

tcatggatct gtatggccaa cccgagcccg tgaaaccctt ccttttctac 350

cgtgccaaga ctggtaggac ctccaccctt gagtctgtgg ccttcccgga 400

ctggttcatt gcctcctcca agagagacca gcccatcatt ctgacttcag 450

aacttgggaa gtcatacaac actgcctttg aattaaatat aaatgactga 500

actcagccta gaggtggcag cttggtcttt gtcttaaagt ttctggttcc 550

caatgtgttt tcgtctacat tttcttagtg tcattttcac gctggtgctg 600

agacaggagc aaggctgctg ttatcatctc attttataat gaagaagaag 650

caattacttc atagcaactg aagaacagga tgtggcctca gaagcaggag 700

agctgggtgg tataaggctg tcctctcaag ctggtgctgt gtaggccaca 750

aggcatctgc atgagtgact ttaagactca aagaccaaac actgagcttt 800

cttctagggg tgggtatgaa gatgcttcag agctcatgcg cgttacccac 850

gatggcatga ctagcacaga gctgatctct gtttctgttt tgctttattc 900

cctcttggga tgatatcatc cagtctttat atgttgccaa tatacctcat 950

tgtgtgtaat agaaccttct tagcattaag accttgtaaa caaaaataat 1000

tcttggggtg ggtatgaaga tgcttcagag ctcatgcgcg ttacccacga 1050

tggcatgact agcacagagc tgatctctgt ttctgttttg ctttattccc 1100

tcttgggatg atatcatcca gtctttatat gttgccaata tacctcattg 1150

tgtgtaatag aaccttctta gcattaagac cttgtaaaca aaaataattc 1200

ttgtgttaag ttaaatcatt tttgtcctaa ttgtaatgtg taatcttaaa 1250

gttaaataaa ctttgtgtat ttatataata ataaagctaa aactgatata 1300

aaataaagaa agagtaaact g 1321

<210> 63
<211> 134
<212> PRT
<213> Homo Sapien

<400> 63

Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val
1 5 10 15

Tyr Gln Ser Ile Thr Val Ala Val Ile Thr Cys Lys Tyr Pro Glu
20 25 30

Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
35 40 45

Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro
50 55 60

Thr Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln
65 70 75

Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly
80 85 90

Arg Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile
95 100 105

Ala Ser Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu
110 115 120

Gly Lys Ser Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp
125 130

<210> 64
<211> 999
<212> DNA
<213> Homo Sapien

<400> 64
gcgaggctgc accagcgcct ggcaccatga ggacgcctgg gcctctgccc 50

gtgctgctgc tgctcctggc gggagccccc gccgcgcggc ccactccccc 100

gacctgctac tcccgcatgc gggccctgag ccaggagatc acccgcgact 150

tcaacctcct gcaggtctcg gagccctcgg agccatgtgt gagatacctg 200

cccaggctgt acctggacat acacaattac tgtgtgctgg acaagctgcg 250

ggactttgtg gcctcgcccc cgtgttggaa agtggcccag gtagattcct 300

tgaaggacaa agcacggaag ctgtacacca tcatgaactc gttctgcagg 350

agagatttgg tattcctgtt ggatgactgc aatgccttgg aatacccaat 400

cccagtgact acggtcctgc cagatcgtca gcgctaaggg aactgagacc 450

agagaaagaa cccaagagaa ctaaagttat gtcagctacc cagacttaat 500

gggccagagc catgaccctc acaggtcttg tgttagttgt atctgaaact 550

gttatgtatc tctctacctt ctggaaaaca gggctggtat tcctacccag 600

gaacctcctt tgagcataga gttagcaacc atgcttctca ttcccttgac 650

tcatgtcttg ccaggatggt tagatacaca gcatgttgat ttggtcacta 700

aaaagaagaa aaggactaac aagcttcact tttatgaaca actattttga 750

gaacatgcac aatagtatgt ttttattact ggtttaatgg agtaatggta 800

cttttattct ttcttgatag aaacctgctt acatttaacc aagcttctat 850

tatgcctttt tctaacacag actttcttca ctgtctttca tttaaaaaga 900

aattaatgct cttaagatat atattttacg tagtgctgac aggacccact 950

ctttcattga aaggtgatga aaatcaaata aagaatctct tcacatgga 999

<210> 65
<211> 136
<212> PRT
<213> Homo Sapien

<400> 65

Met	Arg	Thr	Pro	Gly	Pro	Leu	Pro	Val	Leu	Leu	Leu	Leu	Leu	Ala	
1				5					10						15
Gly	Ala	Pro	Ala	Ala	Arg	Pro	Thr	Pro	Pro	Thr	Cys	Tyr	Ser	Arg	
				20					25						30
Met	Arg	Ala	Leu	Ser	Gln	Glu	Ile	Thr	Arg	Asp	Phe	Asn	Leu	Leu	
				35					40						45
Gln	Val	Ser	Glu	Pro	Ser	Glu	Pro	Cys	Val	Arg	Tyr	Leu	Pro	Arg	
				50					55						60
Leu	Tyr	Leu	Asp	Ile	His	Asn	Tyr	Cys	Val	Leu	Asp	Lys	Leu	Arg	
				65					70						75
Asp	Phe	Val	Ala	Ser	Pro	Pro	Cys	Trp	Lys	Val	Ala	Gln	Val	Asp	
				80					85						90
Ser	Leu	Lys	Asp	Lys	Ala	Arg	Lys	Leu	Tyr	Thr	Ile	Met	Asn	Ser	
				95					100						105
Phe	Cys	Arg	Arg	Asp	Leu	Val	Phe	Leu	Leu	Asp	Asp	Cys	Asn	Ala	
				110					115						120
Leu	Glu	Tyr	Pro	Ile	Pro	Val	Thr	Thr	Val	Leu	Pro	Asp	Arg	Gln	
				125					130						135

Arg

<210> 66
<211> 1893
<212> DNA
<213> Homo Sapien

<400> 66
gtctccgcgt cacaggaact tcagcaccca cagggcggac agcgctcccc 50

tctacctgga gacttgactc ccgcgcgccc caaccctgct tatcccttga 100

ccgtcgagtg tcagagatcc tgcagccgcc cagtcccggc ccctctcccg 150

ccccacaccc accctcctgg ctcttcctgt ttttactcct ccttttcatt 200

cataacaaaa gctacagctc caggagccca gcgccgggct gtgacccaag 250

ccgagcgtgg aagaatgggg ttcctcggga ccggcacttg gattctggtg 300

ttagtgctcc cgattcaagc tttccccaaa cctggaggaa gccaagacaa 350

atctctacat aatagagaat taagtgcaga aagacctttg aatgaacaga 400

ttgctgaagc agaagaagac aagattaaaa aaacatatcc tccagaaaac 450

aagccaggtc agagcaacta ttcttttgtt gataacttga acctgctaaa 500

ggcaataaca gaaaaggaaa aaattgagaa agaaagacaa tctataagaa 550

gctccccact tgataataag ttgaatgtgg aagatgttga ttcaaccaag 600

aatcgaaaac tgatcgatga ttatgactct actaagagtg gattggatca 650

taaatttcaa gatgatccag atggtcttca tcaactagac gggactcctt 700

taaccgctga agacattgtc cataaaatcg ctgccaggat ttatgaagaa 750

aatgacagag ccgtgtttga caagattgtt tctaaactac ttaatctcgg 800

ccttatcaca gaaagccaag cacatacact ggaagatgaa gtagcagagg 850

ttttacaaaa attaatctca aaggaagcca acaattatga ggaggatccc 900

aataagccca caagctggac tgagaatcag gctggaaaaa taccagagaa 950

agtgactcca atggcagcaa ttcaagatgg tcttgctaag ggagaaaacg 1000

atgaaacagt atctaacaca ttaaccttga caaatggctt ggaaaggaga 1050

actaaaacct acagtgaaga caactttgag gaactccaat atttcccaaa 1100

tttctatgcg ctactgaaaa gtattgattc agaaaaagaa gcaaaagaga 1150

aagaaacact gattactatc atgaaaacac tgattgactt tgtgaagatg 1200

atggtgaaat atggaacaat atctccagaa gaaggtgttt cctaccttga 1250

aaacttggat gaaatgattg ctcttcagac caaaaacaag ctagaaaaaa 1300

atgctactga caatataagc aagcttttcc cagcaccatc agagaagagt 1350

catgaagaaa cagacagtac caaggaagaa gcagctaaga tggaaaagga 1400

atatggaagc ttgaaggatt ccacaaaaga tgataactcc aacccaggag 1450

gaaagacaga tgaacccaaa ggaaaaacag aagcctattt ggaagccatc 1500

agaaaaaata ttgaatggtt gaagaaacat gacaaaaagg gaaataaaga 1550

agattatgac ctttcaaaga tgagagactt catcaataaa caagctgatg 1600

cttatgtgga gaaaggcatc cttgacaagg aagaagccga ggccatcaag 1650

cgcatttata gcagcctgta aaaatggcaa aagatccagg agtctttcaa 1700

ctgtttcaga aaacataata tagcttaaaa cacttctaat tctgtgatta 1750

aaatttttg acccaagggt tattagaaag tgctgaattt acagtagtta 1800

acctttttaca agtggttaaa acatagcttt cttcccgtaa aaactatctg 1850

aaagtaaagt tgtatgtaag ctgaaaaaaa aaaaaaaaaa aaa 1893

<210> 67
<211> 468
<212> PRT
<213> Homo Sapien

<400> 67

Met Gly Phe Leu Gly Thr Gly Thr Trp Ile Leu Val Leu Val Leu
1 5 10 15

Pro Ile Gln Ala Phe Pro Lys Pro Gly Gly Ser Gln Asp Lys Ser
20 25 30

Leu His Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln
35 40 45

Ile Ala Glu Ala Glu Glu Asp Lys Ile Lys Lys Thr Tyr Pro Pro
50 55 60

Glu Asn Lys Pro Gly Gln Ser Asn Tyr Ser Phe Val Asp Asn Leu
65 70 75

Asn Leu Leu Lys Ala Ile Thr Glu Lys Glu Lys Ile Glu Lys Glu
80 85 90

Arg Gln Ser Ile Arg Ser Ser Pro Leu Asp Asn Lys Leu Asn Val
95 100 105

Glu Asp Val Asp Ser Thr Lys Asn Arg Lys Leu Ile Asp Asp Tyr
110 115 120

Asp Ser Thr Lys Ser Gly Leu Asp His Lys Phe Gln Asp Asp Pro
125 130 135

Asp Gly Leu His Gln Leu Asp Gly Thr Pro Leu Thr Ala Glu Asp
140 145 150

Ile Val His Lys Ile Ala Ala Arg Ile Tyr Glu Glu Asn Asp Arg
155 160 165

Ala Val Phe Asp Lys Ile Val Ser Lys Leu Leu Asn Leu Gly Leu
170 175 180

Ile Thr Glu Ser Gln Ala His Thr Leu Glu Asp Glu Val Ala Glu
185 190 195

Val Leu Gln Lys Leu Ile Ser Lys Glu Ala Asn Asn Tyr Glu Glu
200 205 210

Asp Pro Asn Lys Pro Thr Ser Trp Thr Glu Asn Gln Ala Gly Lys
215 220 225

Ile Pro Glu Lys Val Thr Pro Met Ala Ala Ile Gln Asp Gly Leu
230 235 240

Ala Lys Gly Glu Asn Asp Glu Thr Val Ser Asn Thr Leu Thr Leu
245 250 255

Thr Asn Gly Leu Glu Arg Arg Thr Lys Thr Tyr Ser Glu Asp Asn
260 265 270

Phe Glu Glu Leu Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Lys
275 280 285

Ser Ile Asp Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile
290 295 300

Thr Ile Met Lys Thr Leu Ile Asp Phe Val Lys Met Met Val Lys
305 310 315

Tyr Gly Thr Ile Ser Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn
320 325 330

Leu Asp Glu Met Ile Ala Leu Gln Thr Lys Asn Lys Leu Glu Lys
335 340 345

Asn Ala Thr Asp Asn Ile Ser Lys Leu Phe Pro Ala Pro Ser Glu
350 355 360

Lys Ser His Glu Glu Thr Asp Ser Thr Lys Glu Glu Ala Ala Lys
365 370 375

Met Glu Lys Glu Tyr Gly Ser Leu Lys Asp Ser Thr Lys Asp Asp
380 385 390

Asn Ser Asn Pro Gly Gly Lys Thr Asp Glu Pro Lys Gly Lys Thr
395 400 405

Glu Ala Tyr Leu Glu Ala Ile Arg Lys Asn Ile Glu Trp Leu Lys
410 415 420

Lys His Asp Lys Lys Gly Asn Lys Glu Asp Tyr Asp Leu Ser Lys
425 430 435

Met Arg Asp Phe Ile Asn Lys Gln Ala Asp Ala Tyr Val Glu Lys
440 445 450

Gly Ile Leu Asp Lys Glu Glu Ala Glu Ala Ile Lys Arg Ile Tyr
455 460 465

Ser Ser Leu

<210> 68
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 68
cgtcacagga acttcagcac cc 22

<210> 69
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 69
gtcttggctt cctccaggtt tgg 23

<210> 70
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
ggacagcgct cccctctacc tggagacttg actcccgc 38

<210> 71
<211> 2379
<212> DNA
<213> Homo Sapien

<400> 71
gttgctccgg cggcgctcgg ggagggagcc agcagcctag ggcctaggcc 50

cgggccacca tggcgctgcc tccaggccca gccgccctcc ggcacacact 100

gctgctcctg ccagcccttc tgagctcagg ttgggggggag ttggagccac 150

aaatagatgg tcagacctgg gctgagcggg cacttcggga gaatgaacgc 200

cacgccttca cctgccgggt ggcaggggggg cctggcaccc ccagattggc 250

ctggtatctg gatggacagc tgcaggaggc cagcacctca agactgctga 300

gcgtgggagg ggaggccttc tctggaggca ccagcacctt cactgtcact 350

gcccatcggg cccagcatga gctcaactgc tctctgcagg accccagaag 400

tggccgatca gccaacgcct ctgtcatcct taatgtgcaa ttcaagccag 450

agattgccca agtcggcgcc aagtaccagg aagctcaggg cccaggcctc 500

ctggttgtcc tgtttgccct ggtgcgtgcc aacccgccgg ccaatgtcac 550

ctggatcgac caggatgggc cagtgactgt caacacctct gacttcctgg 600

tgctggatgc gcagaactac ccctggctca ccaaccacac ggtgcagctg 650

cagctccgca gcctggcaca caacctctcg gtggtggcca ccaatgacgt 700

gggtgtcacc agtgcgtcgc ttccagcccc aggcccctcc cggcacccat 750

ctctgatatc aagtgactcc aacaacctaa aactcaacaa cgtgcgcctg 800

ccacgggaga acatgtccct cccgtccaac cttcagctca atgacctcac 850

tccagattcc agagcagtga aaccagcaga ccggcagatg gctcagaaca 900

acagccggcc agagcttctg gacccggagc ccggcggcct cctcaccagc 950

caaggtttca tccgcctccc agtgctgggc tatatctatc gagtgtccag 1000

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tctcttggcc tctggacacc ctcccattcc tccaaggcat cctctaccta 1100

gctaggtcac caacgtgaag aagttatgcc actgccactt ttgcttgccc 1150

tcctggctgg ggtgccctcc atgtcatgca cgtgatgcat ttcactgggc 1200

tgtaacccgc aggggcacag gtatctttgg caaggctacc agttggacgt 1250

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tgtacagtag gcatgggggc gtgcctgtgt gggggacagg gagggccctg 1450

catggatttt cctccttcct atgctatgta gccttgttcc ctcaggtaaa 1500

atttaggacc ctgctagctg tgcagaaccc aattgccctt tgcacagaaa 1550

ccaacccctg acccagcggt accggccaag cacaaacgtc ctttttgctg 1600

cacacgtctc tgcccttcac ttcttctctt ctgtccccac ctcctcttgg 1650

gaattctagg ttacacgttg gaccttctct actacttcac tgggcactag 1700

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ggtgagtgag gggcccagag ccctctttgt ggcttcccca cgtttggcct 1900

tctgggattc actgtgagtg tcctgagctc tcggggttga tggtttttct 1950

ctcagcatgt ctcctccacc acgggacccc agccctgacc aacccatggt 2000

tgcctcatca gcaggaaggt gcccttcctg gaggatggtc gccacaggca 2050

cataattcaa cagtgtggaa gctttagggg aacatggaga aagaaggaga 2100

ccacataccc caaagtgacc taagaacact ttaaaaagca acatgtaaat 2150

gattggaaat taatatagta cagaatatat ttttcccttg ttgagatctt 2200

cttttgtaat gtttttcatg ttactgccta gggcggtgct gagcacacag 2250

caagtttaat aaacttgact gaattcattt aaaaaaaaaa aaaaaaaaaa 2300

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2350

aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 2379

<210> 72
<211> 322
<212> PRT
<213> Homo Sapien

<400> 72

Met	Ala	Leu	Pro	Pro	Gly	Pro	Ala	Ala	Leu	Arg	His	Thr	Leu	Leu	
1				5				10						15	
Leu	Leu	Pro	Ala	Leu	Leu	Ser	Ser	Gly	Trp	Gly	Glu	Leu	Glu	Pro	
			20					25					30		
Gln	Ile	Asp	Gly	Gln	Thr	Trp	Ala	Glu	Arg	Ala	Leu	Arg	Glu	Asn	
			35					40					45		
Glu	Arg	His	Ala	Phe	Thr	Cys	Arg	Val	Ala	Gly	Gly	Pro	Gly	Thr	
			50					55					60		
Pro	Arg	Leu	Ala	Trp	Tyr	Leu	Asp	Gly	Gln	Leu	Gln	Glu	Ala	Ser	
			65					70					75		
Thr	Ser	Arg	Leu	Leu	Ser	Val	Gly	Gly	Glu	Ala	Phe	Ser	Gly	Gly	
			80					85					90		
Thr	Ser	Thr	Phe	Thr	Val	Thr	Ala	His	Arg	Ala	Gln	His	Glu	Leu	
			95					100					105		
Asn	Cys	Ser	Leu	Gln	Asp	Pro	Arg	Ser	Gly	Arg	Ser	Ala	Asn	Ala	
			110					115					120		
Ser	Val	Ile	Leu	Asn	Val	Gln	Phe	Lys	Pro	Glu	Ile	Ala	Gln	Val	
			125					130					135		
Gly	Ala	Lys	Tyr	Gln	Glu	Ala	Gln	Gly	Pro	Gly	Leu	Leu	Val	Val	
			140					145					150		
Leu	Phe	Ala	Leu	Val	Arg	Ala	Asn	Pro	Pro	Ala	Asn	Val	Thr	Trp	
			155					160					165		

Ile Asp Gln Asp Gly Pro Val Thr Val Asn Thr Ser Asp Phe Leu
170 175 180

Val Leu Asp Ala Gln Asn Tyr Pro Trp Leu Thr Asn His Thr Val
185 190 195

Gln Leu Gln Leu Arg Ser Leu Ala His Asn Leu Ser Val Val Ala
200 205 210

Thr Asn Asp Val Gly Val Thr Ser Ala Ser Leu Pro Ala Pro Gly
215 220 225

Pro Ser Arg His Pro Ser Leu Ile Ser Ser Asp Ser Asn Asn Leu
230 235 240

Lys Leu Asn Asn Val Arg Leu Pro Arg Glu Asn Met Ser Leu Pro
245 250 255

Ser Asn Leu Gln Leu Asn Asp Leu Thr Pro Asp Ser Arg Ala Val
260 265 270

Lys Pro Ala Asp Arg Gln Met Ala Gln Asn Asn Ser Arg Pro Glu
275 280 285

Leu Leu Asp Pro Glu Pro Gly Gly Leu Leu Thr Ser Gln Gly Phe
290 295 300

Ile Arg Leu Pro Val Leu Gly Tyr Ile Tyr Arg Val Ser Ser Val
305 310 315

Ser Ser Asp Glu Ile Trp Leu
320

<210> 73
<211> 843
<212> DNA
<213> Homo Sapien

<400> 73
cggggacgga agcggcccct gggcccgagg ggctggagcc gggccggggc 50

gatgtggagc gcgggccgcg gcggggctgc ctggccggtg ctgttggggc 100

tgctgctggc gctgttagtg ccgggcggtg gtgccgccaa gaccggtgcg 150

gagctcgtga cctgcgggtc ggtgctgaag ctgctcaata cgcaccaccg 200

cgtgcggctg cactcgcacg acatcaaata cggatccggc agcggccagc 250

aatcggtgac cggcgtagag gcgtcggacg acgccaatag ctactggcgg 300

atccgcggcg gctcggaggg cgggtgcccg cgcgggtccc cggtgcgctg 350

cgggcaggcg gtgaggctca cgcatgtgct tacgggcaag aacctgcaca 400

cgcaccactt cccgtcgccg ctgtccaaca accaggaggt gagtgccttt 450

ggggaagacg gcgagggcga cgacctggac ctatggacag tgcgctgctc 500

tggacagcac tgggagcgtg aggctgctgt gcgcttccag catgtgggca 550

cctctgtgtt cctgtcagtc acgggtgagc agtatggaag ccccatccgt 600

gggcagcatg aggtccacgg catgcccagt gccaacacgc acaatacgtg 650

gaaggccatg gaaggcatct tcatcaagcc tagtgtggag ccctctgcag 700

gtcacgatga actctgagtg tgtggatgga tgggtggatg gagggtggca 750

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gtcctcaagt gcctttgtga ttaaagaatg ttggtctatg aaa 843

<210> 74
<211> 221
<212> PRT
<213> Homo Sapien

<400> 74

Met	Trp	Ser	Ala	Gly	Arg	Gly	Gly	Ala	Ala	Trp	Pro	Val	Leu	Leu
1				5				10						15
Gly	Leu	Leu	Leu	Ala	Leu	Leu	Val	Pro	Gly	Gly	Gly	Ala	Ala	Lys
				20				25						30
Thr	Gly	Ala	Glu	Leu	Val	Thr	Cys	Gly	Ser	Val	Leu	Lys	Leu	Leu
				35				40						45
Asn	Thr	His	His	Arg	Val	Arg	Leu	His	Ser	His	Asp	Ile	Lys	Tyr
				50				55						60
Gly	Ser	Gly	Ser	Gly	Gln	Gln	Ser	Val	Thr	Gly	Val	Glu	Ala	Ser
				65				70						75
Asp	Asp	Ala	Asn	Ser	Tyr	Trp	Arg	Ile	Arg	Gly	Gly	Ser	Glu	Gly
				80				85						90
Gly	Cys	Pro	Arg	Gly	Ser	Pro	Val	Arg	Cys	Gly	Gln	Ala	Val	Arg
				95				100						105
Leu	Thr	His	Val	Leu	Thr	Gly	Lys	Asn	Leu	His	Thr	His	His	Phe
				110				115						120
Pro	Ser	Pro	Leu	Ser	Asn	Asn	Gln	Glu	Val	Ser	Ala	Phe	Gly	Glu
				125				130						135
Asp	Gly	Glu	Gly	Asp	Asp	Leu	Asp	Leu	Trp	Thr	Val	Arg	Cys	Ser
				140				145						150
Gly	Gln	His	Trp	Glu	Arg	Glu	Ala	Ala	Val	Arg	Phe	Gln	His	Val
				155				160						165
Gly	Thr	Ser	Val	Phe	Leu	Ser	Val	Thr	Gly	Glu	Gln	Tyr	Gly	Ser
				170				175						180
Pro	Ile	Arg	Gly	Gln	His	Glu	Val	His	Gly	Met	Pro	Ser	Ala	Asn
				185				190						195

Thr His Asn Thr Trp Lys Ala Met Glu Gly Ile Phe Ile Lys Pro
200 205 210

Ser Val Glu Pro Ser Ala Gly His Asp Glu Leu
215 220

<210> 75
<211> 1049
<212> DNA
<213> Homo Sapien

<400> 75
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ttggaaccac agacgtgagc cactccaccc agcctaaaac ttcatcttct 100

ttggatgaga tgaacacttt taacaagaga acaggactct atataaatcg 150

ctgtgggctc accacctcta aggaggagca ctgactgaag acagaaaaat 200

tgatgaactg aagaagacat ggtccattat gccttacaaa cttacacagt 250

gctttgggaa ttccaaagta ctcagtggag agaggtgttt caggagccgt 300

agagccagat cgtcatcatg tctgcattgt ggctgctgct gggcctcctt 350

gccctgatgg acttgtctga aagcagcaac tggggatgct atggaaacat 400

ccaaagcctg gacacccctg gagcatcttg tgggattgga agacgtcacg 450

gcctgaacta ctgtggagtt cgtgcttctg aaaggctggc tgaaatagac 500

atgccatacc tcctgaaata tcaacccatg atgcaaacca ttggccaaaa 550

gtactgcatg gatcctgccg tgatcgctgg tgtcttgtcc aggaagtctc 600

ccggtgacaa aattctggtc aacatgggcg ataggactag catggtgcag 650

gaccctggct ctcaagctcc cacatcctgg attagtgagt ctcaggtttc 700

ccagacaact gaagttctga ctactagaat caaagaaatc cagaggaggt 750

ttccaacctg gacccctgac cagtacctga gaggtggact ctgtgcctac 800

agtgggggtg ctggctatgt ccgaagcagc caggacctga gctgtgactt 850

ctgcaatgat gtccttgcac gagccaagta cctcaagaga catggcttct 900

aacatctcag atgaaaccca agaccatgat cacatatgca gcctcaaatg 950

ttacacagat aaaactagcc aagggcacct gtaactggga atctgagttt 1000

gacctaaaag tcattaaaat aacatgaatc ccattaaaaa aaaaaaaaa 1049

<210> 76
<211> 194
<212> PRT
<213> Homo Sapien

<400> 76

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Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp
  1               5                  10                  15

Leu Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser
                20                  25                  30

Leu Asp Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly
                35                  40                  45

Leu Asn Tyr Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile
                50                  55                  60

Asp Met Pro Tyr Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile
                65                  70                  75

Gly Gln Lys Tyr Cys Met Asp Pro Ala Val Ile Ala Gly Val Leu
                80                  85                  90

Ser Arg Lys Ser Pro Gly Asp Lys Ile Leu Val Asn Met Gly Asp
                95                 100                 105

Arg Thr Ser Met Val Gln Asp Pro Gly Ser Gln Ala Pro Thr Ser
               110                 115                 120

Trp Ile Ser Glu Ser Gln Val Ser Gln Thr Thr Glu Val Leu Thr
               125                 130                 135

Thr Arg Ile Lys Glu Ile Gln Arg Arg Phe Pro Thr Trp Thr Pro
               140                 145                 150

Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala Tyr Ser Gly Gly Ala
               155                 160                 165

Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys Asp Phe Cys Asn
               170                 175                 180

Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His Gly Phe
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<210> 77
<211> 899
<212> DNA
<213> Homo Sapien

<400> 77

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gtctcagctg acattcgctg tcactcctgc tacaaggtcc ctgtgctggg 150

ctgtgtggac cggcagtcct gccgcctgga gccaggacag caatgcctga 200

caacacatgc ataccttggt aagatgtggg ttttctccaa tctgcgctgt 250

ggcacaccag aagagccctg tcaggaggcc ttcaaccaaa ccaaccgcaa 300
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gctgggtctg acatataaca ccacctgctg caacaaggac aactgcaaca 350

gcgcaggacc ccggcccact ccagccctgg gccttgtctt ccttacctcc 400

ttggctggcc ttggcctctg gctgctgcac tgagactcat tccattggct 450

gcccctcctc ccacctgcct tggcctgagc ctctctccct gtgtctctgt 500

atcccctggc tttacagaat cgtctctccc tagctcccat ttctttaatt 550

aaacactgtt ccgagtggtc tcctcatcca tccttcccac ctcacaccct 600

tcactctcct ttttctgggt cccttcccac ttccttccag gacctccatt 650

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cttgaggagg gattgggatc tgggcctgaa atggggcttc tgtgttgtcc 750

ccagtgaagg ctcccacaag gacctgatga cctcactgta cagagctgac 800

tccccaaacc caggctccca tatgtacccc atcccccata ctcacctctt 850

tccattttga gtaataaatg tctgagtctg gaaaaaaaaa aaaaaaaaa 899

<210> 78
<211> 125
<212> PRT
<213> Homo Sapien

<400> 78

Met	Lys	Ala	Leu	Met	Leu	Leu	Thr	Leu	Ser	Val	Leu	Leu	Cys	Trp
1				5				10						15
Val	Ser	Ala	Asp	Ile	Arg	Cys	His	Ser	Cys	Tyr	Lys	Val	Pro	Val
				20				25						30
Leu	Gly	Cys	Val	Asp	Arg	Gln	Ser	Cys	Arg	Leu	Glu	Pro	Gly	Gln
				35				40						45
Gln	Cys	Leu	Thr	Thr	His	Ala	Tyr	Leu	Gly	Lys	Met	Trp	Val	Phe
				50				55						60
Ser	Asn	Leu	Arg	Cys	Gly	Thr	Pro	Glu	Glu	Pro	Cys	Gln	Glu	Ala
				65				70						75
Phe	Asn	Gln	Thr	Asn	Arg	Lys	Leu	Gly	Leu	Thr	Tyr	Asn	Thr	Thr
				80				85						90
Cys	Cys	Asn	Lys	Asp	Asn	Cys	Asn	Ser	Ala	Gly	Pro	Arg	Pro	Thr
				95				100						105
Pro	Ala	Leu	Gly	Leu	Val	Phe	Leu	Thr	Ser	Leu	Ala	Gly	Leu	Gly
				110				115						120
Leu	Trp	Leu	Leu	His										
				125										

<210> 79

<211> 1977
<212> DNA
<213> Homo Sapien

<400> 79
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tagctgcgca gcgtcgcgcg cgctaccgca cccaggttcg gcccgtaggc 150

gtctggcagc ccggcgccat cttcatcgag cgccatggcc gcagcctgcg 200

ggccgggagc ggccgggtac tgcttgctcc tcggcttgca tttgtttctg 250

ctgaccgcgg gccctgccct gggctggaac gaccctgaca gaatgttgct 300

gcgggatgta aaagctctta ccctccacta tgaccgctat accacctccc 350

gcaggctgga tcccatccca cagttgaaat gtgttggagg cacagctggt 400

tgtgattctt ataccccaaa agtcatacag tgtcagaaca aaggctggga 450

tgggtatgat gtacagtggg aatgtaagac ggacttagat attgcataca 500

aatttggaaa aactgtggtg agctgtgaag gctatgagtc ctctgaagac 550

cagtatgtac taagaggttc ttgtggcttg gagtataatt tagattatac 600

agaacttggc ctgcagaaac tgaaggagtc tggaaagcag cacggctttg 650

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ataaagtaga aagttggagt caaacactgg atgcagaaat tttggatttt 1250

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aggggatatt caaaagttct gtggtgttat gtccagtgta gctttttgta 1350

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ttactgtgga atgctaaaaa tacattaatt tctaaaacct gtgatgccct 1500

aagaagcatt aagaatgaag gtgttgtact aatagaaact aagtacagaa 1550

aatttcagtt ttaggtggtt gtagctgatg agttattacc tcatagagac 1600

tataatattc tatttggtat tatattattt gatgtttgct gttcttcaaa 1650

catttaaatc aagctttgga ctaattatgc taatttgtga gttctgatca 1700

cttttgagct ctgaagcttt gaatcattca gtggtggaga tggccttctg 1750

gtaactgaat attaccttct gtaggaaaag gtggaaaata agcatctaga 1800

aggttgttgt gaatgactct gtgctggcaa aaatgcttga aacctctata 1850

tttctttcgt tcataagagg taaaggtcaa atttttcaac aaaagtcttt 1900

taataacaaa agcatgcagt tctctgtgaa atctcaaata ttgttgtaat 1950

agtctgtttc aatcttaaaa agaatca 1977

<210> 80
<211> 339
<212> PRT
<213> Homo Sapien

<400> 80

Met	Ala	Ala	Ala	Cys	Gly	Pro	Gly	Ala	Ala	Gly	Tyr	Cys	Leu	Leu	
1				5				10						15	
Leu	Gly	Leu	His	Leu	Phe	Leu	Leu	Thr	Ala	Gly	Pro	Ala	Leu	Gly	
				20				25						30	
Trp	Asn	Asp	Pro	Asp	Arg	Met	Leu	Leu	Arg	Asp	Val	Lys	Ala	Leu	
				35				40						45	
Thr	Leu	His	Tyr	Asp	Arg	Tyr	Thr	Thr	Ser	Arg	Arg	Leu	Asp	Pro	
				50				55						60	
Ile	Pro	Gln	Leu	Lys	Cys	Val	Gly	Gly	Thr	Ala	Gly	Cys	Asp	Ser	
				65				70						75	
Tyr	Thr	Pro	Lys	Val	Ile	Gln	Cys	Gln	Asn	Lys	Gly	Trp	Asp	Gly	
				80				85						90	
Tyr	Asp	Val	Gln	Trp	Glu	Cys	Lys	Thr	Asp	Leu	Asp	Ile	Ala	Tyr	
				95				100						105	
Lys	Phe	Gly	Lys	Thr	Val	Val	Ser	Cys	Glu	Gly	Tyr	Glu	Ser	Ser	
				110				115						120	
Glu	Asp	Gln	Tyr	Val	Leu	Arg	Gly	Ser	Cys	Gly	Leu	Glu	Tyr	Asn	
				125				130						135	

Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys Leu Lys Glu Ser Gly
140 145 150

Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr Tyr Tyr Lys Trp
155 160 165

Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile Thr Ile Val
170 175 180

Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser
185 190 195

Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe
200 205 210

Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
215 220 225

Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
230 235 240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly
245 250 255

Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly
260 265 270

Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro
275 280 285

Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro
290 295 300

Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly
305 310 315

Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala
320 325 330

Ser Gly Tyr Gly Gly Thr Arg Arg Arg
335